

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 1, 2001, 15:52:28 ; Search time 170.72 Seconds  
(without alignments)  
17.898 Million cell updates/sec

Title: US-09-331-631A-3\_COPY\_29\_73

Perfect score: 252  
Sequence: 1 SEFROEXECKRQCMQLET.....RCVSQCDKRFEDIDMSKYD 45

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR\_66:\*\*\*  
2: PIR1:\*\*\*  
3: PIR2:\*\*\*  
4: PIR3:\*\*\*  
5: PIR4:\*\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77.5	30.8	509	2 S08059	alpha-globulin typ
2	77.5	30.8	588	1 FMCNAB	alpha-globulin B p
3	72	28.6	605	2 S06398	alpha-globulin typ
4	70.5	28.0	566	2 S22477	vicillin precursor
5	67.5	26.8	47	2 JC3557	arginine/glutamate
6	67	26.6	810	2 T44430	protein PV100 [imp
7	67	26.6	1170	1 TSHUP1	thrombospondin 1 p
8	67	26.6	1170	2 A40558	thrombospondin 1 p
9	64	25.4	554	2 T45840	GTPase activating
10	63	25.0	524	2 J01730	62k sucrose-bindin
11	59.5	23.6	3078	2 T28432	variant-specific s
12	58	23.0	242	2 T29699	hypothetical prote
13	58	23.0	1421	2 T05892	hypothetical prote
14	57	22.6	316	2 G71600	refin PEB105w - m
15	57	22.6	725	1 MMV294	A-type inclusion p
16	57	22.6	726	2 JQ2162	A-type inclusion p
17	57	22.6	1284	1 MWV2AT	A-type inclusion p
18	55	21.8	308	2 B55346	phosphoprotein pho
19	55	21.8	345	2 A71601	refin PEB1015w - m
20	55	21.8	623	2 T06674	hypothetical prote
21	55	21.8	795	1 HHC08	heat shock protei
22	55	21.8	822	2 T02824	hypothetical prote
23	54.5	21.6	244	2 S44822	F44E2.3 protein -
24	54.5	21.6	1021	2 T15765	hypothetical prote
25	54.5	21.6	1259	2 T132901	hypothetical prote
26	54.5	21.6	2715	2 T13049	eyelid - fruit fly
27	54	21.4	291	2 S62730	cyclin D1 - zebra
28	54	21.4	314	2 T02964	cyclin A-type (cto
29	54	21.4	643	2 T19225	Ro autoantigen 60k

30	54	21.4	880	2 F75103	probable purine NT
31	53.5	21.2	67	2 T15592	hypothetical prote
32	53.5	21.2	301	2 I54209	hypothetical prote
33	53.5	21.2	1642	2 T08880	NMDA receptor-bind
34	53	21.0	622	2 E69006	glutamate synthase
35	53	21.0	702	2 S46854	A28L protein - var
36	53	21.0	702	2 B72167	A29L protein - var
37	53	21.0	702	2 T28570	hypothetical prote
38	53	21.0	795	2 I50255	108k heat shock pr
39	52.5	20.8	91	1 S00219	ubiquinol--cytochr
40	52.5	20.8	96	1 XLH0A	collipase A precurs
41	52.5	20.8	275	2 B81430	probable prephenat
42	52.5	20.8	425	2 T18592	hypothetical prote
43	52.5	20.8	600	2 T18593	hypothetical prote
44	52.5	20.8	1172	1 TSHUP2	thrombospondin 2 p
45	52	20.6	33	2 A41822	antimicrobial pept

#### ALIGNMENTS

##### RESULT 1

S08059

alpha-globulin type B precursor (clone C72) - upland cotton (fragment)

N:Alternate names: seed storage protein

C:Species: Gossypium hirsutum (upland cotton)

C>Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 30-Sep-1993

C:Accession: S08059

R:Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.

Plant Mol. Biol. 9, 533-546, 1987

A:Title: Developmental biochemistry of cottonseed embryogenesis and germination. XIX.

A:Reference number: S06398

A:Accession: S08059

A>Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-509 <CHL>

C:Superfamily: glycinn

Query Match 30.8%; Score 77.5; DB 2; Length 509;

Best Local Similarity 41.2%; Pred. No. 0.11;

Matches 14; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

QY 5 RQRYEEDCKRQCMQLETSGQWRRCVSQCDKRFED 38

DB 3 QRRYEECGQECRQGF-ERQPPQCGRCRKRFEGE 35

##### RESULT 2

FMCNAB

alpha-globulin B precursor (clone C72) - upland cotton

N:Alternate names: seed storage protein; vicillin precursor

C:Species: Gossypium hirsutum (upland cotton)

C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Jul-1999

C:Accession: A30838; S06911

R:Chlan, C.A.; Pyle, J.B.; Legocki, A.B.; Dure III, L.

Plant Mol. Biol. 7, 475-489, 1986

A:Title: Developmental biochemistry of cottonseed embryogenesis and germination XVIII

A:Reference number: A30838

A:Accession: A30838

A:Molecule type: mRNA

A:Residues: 1-588 <CHL>

A:Cross-references: GB:M16891; NID:q167374; PID:AAA33071.1; PID:q167375

A:Experimental source: var. Coker 201

R:Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.

Plant Mol. Biol. 9, 533-546, 1987

A:Title: Developmental biochemistry of cottonseed embryogenesis and germination. XIX.

A:Reference number: S06398

A:Accession: S06911

A>Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-81 <CH2>

C:Comment: This is a seed storage protein.



A:Cross-references: GB:J04665; NID:937137; PIDN:CAA28370.1; PID:937738  
A:Note: parts of this sequence, including the amino end of the mature protein, were determined by R. Laherty, C.D.; Gierman, T.M.; Dixit, V.M.  
J. Biol. Chem. 264, 11222-11227, 1989  
A:Title: Characterization of the promoter region of the human thrombospondin gene. DNA  
A:Reference number: A34274; MUID:89291870  
A:Accession: A34274  
A:Molecule type: DNA  
A:Residues: 1-166 <LAH>  
A:Cross-references: GB:J04835  
R.Hennessy, S.W.; Frazier, B.A.; Kim, D.D.; Deckwerth, T.L.; Baumgaertel, D.M.; Rotwein, J. Cell Biol. 108, 729-736, 1989  
A:Title: Complete thrombospondin mRNA sequence includes potential regulatory sites in the  
A:Reference number: A30140; MUID:89139590  
A:Accession: A30140  
A:Molecule type: mRNA  
A:Residues: 1-83, 'A', 85-522, 'A', 524-1170 <HEN>  
A:Cross-references: EMBL:X14787; NID:937464; PIDN:CAA32889.1; PID:937465  
A:Note: parts of this sequence, including the amino end of the mature protein, were determined by R.Kohayashi, S.; Eden-McCutchan, F.; Framson, P.; Bornstein, P. Biochemistry 23, 8418-8425, 1986  
A:Title: Partial amino acid sequence of human thrombospondin as determined by analysis of  
A:Reference number: A25812; MUID:87157592  
A:Accession: A25812  
A:Molecule type: mRNA  
A:Residues: 1-83, 'A', 85-397 <KOB>  
A:Cross-references: GB:M25631; NID:9538353; PIDN:AAA36741.1; PID:9538354  
R.Dixit, V.M.; Hennessy, S.W.; Grant, G.A.; Rotwein, P.; Frazier, W.A. Proc. Natl. Acad. Sci. U.S.A. 83, 5449-5453, 1986  
A:Reference number: A05172; MUID:86287276  
A:Accession: A05172  
A:Molecule type: mRNA  
A:Residues: 1-83, 'A', 85-374, 'RC' <DIX>  
A:Cross-references: GB:M14326; NID:9340005; PIDN:AAA61237.1; PID:9553801  
A:Note: parts of this sequence, including the amino end of the mature protein, were determined by R.Sun, X.; Skorstengaard, K.; Mosher, D.F. J. Cell Biol. 118, 693-701, 1992  
A:Title: Disulfides modulate RGD-inhibitable cell adhesive activity of thrombospondin.  
A:Reference number: A42927; MUID:92348511  
A:Accession: A42927  
A:Molecule type: protein  
A:Residues: 987-1003 <SUN>  
A:Note: Cys-992 is shown to have a free sulfhydryl  
A:Genetics:  
A:Gene: GDB:THBS1; TSP1; TSP  
A:Cross-references: GDB:120438; OMIM:188060  
A:Map position: 15q15-15q15  
A:Introns: 23/1  
A:Note: the list of introns may be incomplete  
C:Complex: homotrimer, disulfide linked  
C:Function:  
A:Description: participates in cell migration and adhesion, and in platelet aggregation  
C:Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; von  
C:Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer  
E:1-18/Domain: signal sequence #status predicted <SIG>  
E:19-1170/Product: thrombospondin 1 #status predicted <MAT>  
F:317-375/Domain: von Willebrand factor type C repeat homology <WVC>  
F:378-429/Domain: thrombospondin type 1 repeat homology <THRA>  
F:434-490/Domain: thrombospondin type 1 repeat homology <THRB>  
F:491-547/Domain: thrombospondin type 1 repeat homology <THRC>  
F:551-586/Domain: EGF homology <EGF1>  
F:650-689/Domain: EGF homology <EGF>  
F:926-928/Region: cell attachment (R-G-D) motif  
F:171-232/Disulfide bonds: #status predicted  
F:248,360,708,1067/Binding site: carbohydrate (Asn) #status predicted  
F:270,274/Disulfide bonds: interchain #status predicted  
F:610/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted  
F:1051/Binding site: carbohydrate (Asn) (covalent) #status absent

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Oy      13 RQCMQLE-----TSGQMRRC-VSQCDKRFEEIDIMSKY 44
Db      404 RSCDSLNRCEGSSVQTRCHIQECDKRFKODGMSHW 441

RESULT      8
A:0558
thrombospondin 1 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 20-Aug-1999
C:Accession: A40558; A37905; B42587; S68787
R:Lavie, J.; Dugnette, M.; Ferro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.
Genomics 11, 587-600, 1991
A:Title: Characterization of the murine thrombospondin gene.
A:Reference number: A40558; MUID:92128941
A:Accession: A40558
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1170 <LAW>
A:Cross-references: GB:M62449; GB:M62450; GB:M62451; GB:M62452; GB:M62453; GB:M62454;
M62455; GB:M62466; GB:M62467; GB:M62468; GB:M62469; GB:M62470; NID:9511867; PIDN:AAAS
R:Bornstein, P.; Alf, D.; Devareyalu, S.; Franson, P.; Li, P.
J. Biol. Chem. 265, 16691-16698, 1990
A:Title: Characterization of the mouse thrombospondin gene and evaluation of the role
A:Reference number: A37905; MUID:90375546
A:Accession: A37905
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-490 <BOR>
A:Cross-references: GB:J05605; GB:J05606; NID:9201991; PIDN:AAA0431.1; PID:9554390
R:laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
J. Biol. Chem. 267, 3274-3281, 1992
A:Title: Characterization of mouse thrombospondin 2 sequence and expression during ce
A:Reference number: A42587; MUID:92147683
A:Accession: B42587
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1152,'P',1154-1170 <LAH>
A:Cross-references: GB:M87276
A:Note: sequence extracted from NCBI backbone (MCHP:01501)
R:Chen, H.; Aeschlimann, D.; Nowlen, J.; Mosher, D.F.
FEBS Lett. 387, 36-41, 1996
A:Title: Expression and initial characterization of recombinant mouse thrombospondin
A:Reference number: S68787; MUID:96234006
A:Accession: S68787
A:Molecule type: protein
A:Residues: 15-26,'X',28-37 <CHE>
C:Complex: homotrimer, disulfide linked
C:Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology;
C:Keywords: calcium binding; glycoprotein; homotrimer
F:1-18/domain: signal sequence #status predicted <SIG>
F:19-1170/Product: thrombospondin 1 #status predicted <MAT>
F:317-375/Domain: von Willebrand factor type C repeat homology <WVC>
F:378-429/Domain: thrombospondin type 1 repeat homology <THR1>
F:434-490/Domain: thrombospondin type 1 repeat homology <THR2>
F:491-547/Domain: thrombospondin type 1 repeat homology <THR3>
F:551-566/Domain: EGF homology <EGF>
F:248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      26.6%; Score 67; DB 2; Length 1170;
Best Local Similarity 39.5%; Pred. No. 3.9;
Matches 15; Conservative 6; Mismatches 11; Indels 6; Gaps 2;

Oy      13 RQCMQLE-----TSGQMRRC-VSQCDKRFEEIDIMSKY 44
Db      404 RSCDSLNRCEGSSVQTRCHIQECDKRFKODGMSHW 441

RESULT      9
A:05840
GTPase activating-like protein - Arabidopsis thaliana

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N:Alternate names: protein F2K15.210
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C:Accession: J45840
R:Reiger, M.; Gabell, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemcke,
submitted to the Protein Sequence Database, January 2000
A:Reference number: 223015
A:Accession: J45840
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-554 <EMB>
A:Cross-references: EMBL:ALJ32956
C:Genetics:
A:Experimental source: cultivar Columbia; BAC clone F2K15
A:Map position: 3
A:Introns: 53/2; 98/3; 115/2; 133/2
A>Note: F2K15.210

Query Match          25.4%; Score 64; DB 2; Length 554;
Best local Similarity 28.2%; Pred. No. 4.5;
Matches 11; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

.Oy      5 ROYEYECRCQCMQLTSGQMRCVSCQCDRFEEIDWMS 43
         ||||| :||| :||: |:: :||: ||:
Db       148 RKEVERLRQCKRLQKHNNGTAKLYNGSETIQDEYDWR 186

RESULT 10
JOI730
62k sucrose-binding protein precursor - soybean
C:Species: Glycine max (soybean)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Aug-1999
C:Accession: JOI730
R:Grimes, H.D.; Overvoorde, P.J.; Ripp, K.; Franceschi, V.R.; Hiltz, W.D.
Plant Cell 4, 1561-1574, 1992
A>Title: A 62-kD sucrose binding protein is expressed and localized in tissues actively
A:Reference number: JOI730; MUID:93104680
A:Accession: JOI730
A:Molecule type: mRNA
A:Residues: 1-524 <GRI>
A:Cross-references: GB:L06038; NID:g1431744; PIDN:AAB03894.1; PID:g170064
C:Superfamily: glycinin
C:Keywords: sugar transport
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-524/Product: 62k sucrose-binding protein #status predicted <MAT>

Query Match          25.0%; Score 63; DB 2; Length 524;
Best local Similarity 38.2%; Pred. No. 5.6;
Matches 13; Conservative 4; Mismatches 15; Indels 2; Gaps 1;

Oy      2 EFDRQEYECRCQCMQLE--TSQGMRCVSQCDSK 33
         ||: | | | | | | | | | | | | | | | |
Db       34 EEEDPELVTCRHQQCCQQQQYYTEGDKRVCLQSCDR 67

RESULT 11
T28432
variant-specific surface protein 1 - malaria parasite (Plasmodium falciparum)
N:Alternate names: erythrocyte membrane binding protein I (EMP1)
C:Species: Plasmodium falciparum
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C:Accession: T28432
R:Su, X.Z.; Heatwole, V.M.; Wertheimer, S.P.; Guinet, F.; Herrfeldt, J.A.; Peterson, D.S.
Cell 82, 89-100, 1995
A>Title: The large diverse gene family var encodes proteins involved in cytoadherence ar
A:Reference number: Z20487; MUID:95330813
A:Accession: T28432
A>Status: preliminary; translated from GR/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-3078 <SNV>
A:Cross-references: EMBL:L40608; NID:g886374; PTD:g886375; PIDN:AAA75396.1

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[illegible]



